6 KG/

	\			
GKÇE-N	2 - 1 B	CINTAP D	LQYISGR GNGRLCS	
CONGGTCD-VGSY-C-CPPGFT	CQHC VNT-GSY-CKC-SG	VNTHGSYK	VNTFGSYYCKCHIGER FINTOGSF CKCKOCYK	V-EC-SG-QC-SSC -NTVGSY-CRCRPRA-P-B-B-B-B-B-B-B-B-B-B-B-B-B-B-B-B-B-B-
-ZIDDNOJ	<u> </u>	COYS C	CPYNRIC	D88-D
IDEC-SNP	-NE <u>C</u> TM	VNECCMIKPRP COHR C	IDEÇASGKVI ÇPYNRUÇ INEÇTMDSHT ÇSHHANÇ	V - E <u>C</u> - SG - Q
Notch(C)	10244(C) 80	95 133	175	CDITACI

NSDSECPLSHDGYCLHDGVCMXFALDKYAGNCVVGYI---GER--CQYRDLKWWELR EGF (C)

Figure 1

GGCTGGAGAA GAAACAGCAA GGGAGTCTGT GAAGCTACAT GCGAALCTGG ATGTAAGTTT GGTGAGTGCG TGGGACCAAA CAAATGCAGA TGCTTTLCAG GATACACCGG GAAAACCTGC AGTCAAGATG TGAATGAGTG TGGAA1GAAA CCCCGGCCAT GCCAACACAG ATGTGTGAAT ACACACGGAA GCTACAAGTG CTTTTGCCTC AGTGGCCACA TGCTCATGCC AGATGCTACG TGTGTGAACT CNAGGACATG TGCCATGATA AACTGTCAGT ATAGCTGTGA AGACACAGAA (SEQ ID NO 1)

GGCTGGAGAA GAAACAGCAA GGGAGTCTGT GAAGCTACAT GCGAACCTGG ATGTAAGTTT GGTGAGTGCG TGGGACCAAA CAAATGCAGA TGCTTTCCAG GATACACCGG GAAAACCTGC AGTCAAGATG TGAATGAGTG TGGAATGAAA CCCCGGCCAT GCCAACACAG ATGTGTGAAT ACACACGGAA GCTACAAGTG CTTTTGCCTC AGTGGCCACA TGCTCATGCC AGATGCTACG TGTGTGAACT CNAGGACATG TGCCATGATA AACTGTCAGT ATAGCTGTGA AGACACAGAA GAAGGGCCAC AGTGCCTGTG TCCATCCTCA GGACTCCGCC TGGCCCCAAA TGGAAGAGAC TGTCTAGATA TTGATGAATG TGCCTCTGGT AAAGTCATCT GTCCCTACAA TCGAAGATGT GTGAACACAT TTGGAAGCTA CTACTGCAAA TGTCACATTG GTTTCGAACT GCAATATATC AGTGGACGAT ATGACTGTAT AGATATAAAT GAATGTACTA TGGATAGCCA TACGTGCAGC CACCATGCCA ATTGCTTCAA TACCCAAGGG TCCTTCAAGT GTAAATGCAA GCAGGGATAT AAAGGCAATG GACTTCGGTG TTCTGCTATC CCTGAAAATT CTGTGAAGGA AGTCCTCAGA GCACCTGGTA CCATCAAAGA CAGAATCAAG AAGTTGCTTG CTCACAAAA CAGCATGAAA AAGAAGGCAA AAATTAAAAA TGTTACCCCA GAACCCACCA GGACTCCTAC CCCTAAGGTG AACTTGCAGC CCTTCAACTA TGAAGAGATA GTTTCCAGAG GCGGGAACTC TCATGGAGGT AAAAAAGGGA ATGAAGAGAA AATGAAAGAG GGGCTTGAGG ATGAGAAAAG AGAAGAGAAA GCCCTGAAGA ATGACATAGA GGAGCGAAGC CTGCGAGGAG ATGTGTTTTT CCCTAAGGTG AATGAAGCAG GTGAATTCGG CCTGATTCTG GTCCAAAGGA AAGCGCTAAC TTCCAAACTG GAACATAAAG ATTTAAATAT CTCGGTYGAC TGCAGCTTCA ATCATGGGAT CTGTGACTGG AAACAGGATA GAGAAGATGA TTTTGACTGG AATCCTGCTG ATCGAGATAA TGCTATTGGC TTCTATATGG CAGTTCCGGC CTTGGCAGGT CACATGAAAG ACATTGGCCG ATTGAAACTT CTCCTACCTG ACCTGCAACC CCAAAGCAAC TTCTGTTTGC TCTTTGATTA CCGGCTGGCC GGAGACAAG TCGGGAAACT TCGAGTGTTT GTGAAAAACA GTAACAATGC CCTGGCATGG GAGAAGACCA CGAGTGAGGA TGAAAAGTGG AAGACAGGGA AAATTCAGTT GTATCAAGGA ACTGATGCTA CCAAAAGCAT CATTTTTGAÁ GCAGAACGTG GCAAGGGCAA AACCGGCGAA ATCGCAGTGG ATGGCGTCTT GCTTGTTTCA GGCTTATGTC CAGATAGCCT TTTATCTGTG GANNNCTGAA TGGTACTATC TTTATATTTG ACTTTGTATG TCAGTTCCCT GGTTTTTTTG ATATTGCATC ATAGGACCTC TGGCATTTTA AAATTACTAG CTGAAAAATT G (SEQ ID NO 2)

Figure 2

GWRRNSKGVCEATCEPGCKFGECVGPNKCRCFPGYTGKTCSQDVNECGMKPRPCQHR CVNTHGSYKCFCLSGHMLMPDATCVNSRTCAMINCQYSCEDTE (SEQ ID NO 3)

GWRRNSKGVCEATCEPGCKFGECVGPNKCRCFPGYTGKTCSQDVNECGMKPRPCQHR CVNTHGSYKCFCLSGHMLMPDATCVNSRTCAMINCQYSCEDTEEGPQCLCPSSGLRLAP NGRDCLDIDECASGKVICPYNRRCVNTFGSYYCKCHIGFELQYISGRYDCIDINECTMDS HTCSHHANCFNTQGSFKCKCKQGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKKLLAH KNSMKKKAKIKNVTPEPTRTPTPKVNLQPFNYEEIVSRGGNSHGGKKGNEEKMKEGLE DEKREEKALKNDIEERSLRGDVFFPKVNEAGEFGLILVQRKALTSKLEHKDLNISVDCSF NHGICDWKQDREDDFDWNPADRDNAIGFYMAVPALAGHMKDIGRLKLLLPDLQPQSN FCLLFDYRLAGDKVGKLRVFVKNSNNALAWEKTTSEDEKWKTGKIQLYQGTDATKSIIF EAERGKGKTGEIAVDGVLLVSGLCPDSLLSVDDXMVLSLYLTLYVSSLVFLILHHRTSGI LKLLAEKL (SEQ ID NO 4)

Figure 4

ACTAGTGATTCCATCCTAATACGACTCACTATAGGGCTCGAGCGGCCGGGCAGGTCTGCAGGGACAGCACCCGGTA ACTCCGAGTGGAGCGGAGGACCCGAGCGGCTGAGGAGAGAGGAGGCGGCGCTTAGCTGCTACGGGGTCCGGCCGCCC CTCCCGAGGGGGCTCAGGAGGAGGAGGAGGACCCGTGCGAGAATGCCTCTGCCCTGGAGCCTTGCGCTCCCGCTGCTG CTCCCTGGGTGGCAGGTGGTTTCGGGAACGCGGCCAGTGCAAGGCATCACGGGTTGTTAGCATCGGCACGTCAGCCTGG GGTCTGTCACTATGGAACTAAACTGGCCTGCTGCTACGGCTGGAGAAGAACAGCAAGGGAGTCTGTGAAGCTACATGCG CAAGATGTGAATGAGTGTGGAATGAAACCCCGGCCATGCCAACACAGATGTGTGAATACACACGGAAGCTACAAGTGCTT TTGCCTCAGTGGCCACATGCTCATGCCAGATGCTACGTGTGTGAACTCTAGGACATGTGCCATGATAAACTGTCAGTATA CTGTGAAGACACAGAAGAAGGGCCACAGTGCCTGTGTCCATCCTCAGGACTCCGCCTGGCCCCAAATGGAAGAGACTGT CTAGATATTGATGAATGTGCCTCTGGTAAAGTCATCTGTCCCTACAATCGAAGATGTGTGAACACATTTGGAAGCTACTA ATAGCCATACGTGCAGCCACCATGCCAATTGCTTCAATACCCAAGGGTCCTTCAAGTGTAAATGCAAGCAGGATATAAA AATCAAGAAGTTGCTTGCTCACAAAAACAGCATGAAAAAGAAGGCAAAAATTAAAAATGTTACCCCAGAACCCACACGA CTCCTACCCCTAAGGTGAACTTGCAGCCCTTCAACTATGAAGAGATAGTTTCCAGAGGCGGGAACTCTCATGGAGGTAAA AAAGGGAATGAAGAGAAAATGAAAGAGGGGCTTGAGGATGAGAAAAGAGAAGAGAAAAGCCCTGAAGAATGACWTAGAGGA CGCTAACTTCCAAACTGGAACATAAAGATTTAAATATCTCGGTTGACTGCAGCTTCAATCATGGGATCTGTGACTGGAAA CAGGATAGAGAAGATGATTTGACTGGAATCCTGCTGATCGAGATAATGCTATTGGCTTATATATGGCAGTTCCGGCCTT GGCAGGTCACAAGAAAACACTGGCCGATTGAAACTTCTCTTACCTGACCTGCAACCCAAAGCAACTTCTGTTTGCTCT TTGATTACCGGCTGGCCGGAGACAAAGTCGGGAAACTTCGAGTGTTTGTGAAAAACAGTAACAATGCCCTGGCATGGGAG AAGACCACGAGTGAGGATGAAAAGTGGAAGACAGGGAAAATTCAGTTGTATCAAGGAACTGATGCTACCAAAAGCATCAT ATAGCCTTTTATCTGTGGATGACTGAATGTTACTATCTTTATATTTGACTTTGTATGTCAGTTCCCTGGTTTTTTTGATA TTGSATCATAGGACCTCTGGCATTTTAAAATTACTAAGCTGAAAAATTGTAATGTACCAACAGAAATTATTATTGTAAGA TGCCTTTMTTGTATAAGATATGCCAATATTTGCTTTAAATATCATATCACTGTATCTTCTCAGTCATTTCTGAATCTTTC GCTTCTCTCTGCAACATTTCTAGAAAATAGAHAAAAAAGCACAGAGAAATGTTTAACTGTTTGACTCTTATGATAGTTTT TGGAAACTATGACATCAAAGATAGACTTTTGCCTAAGTGGCTTAGCTGGGTCTTTCATAGCCAAACTTGTATATTTAAAT (SEQ ID NO: 5)

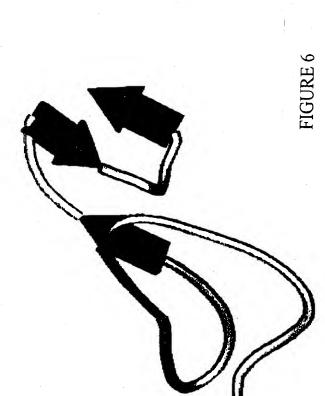
Figure 5

MPLPWSLALPLLIPWVAGGFGNAASARHIGLLASARQPGVCHYGTKLACCYGWRRNSKGVCEATCEPGCKFGECVGPNKC RCFPGYTGKTCSQDVNECGMKPRPCQHRCVNTHGSYKCFCLSGHMLMPDATCVNSRTCAMINCQYSCEDTEEGPQCLCPS SGLRLAPNGRDCLDIDECASGKVICPYNRRCVNTFGSYYCKCHIGFELQYISGRYDCIDINECTMDSHTCSHHANCFNTQ GSFKCKCKQGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKKLLAHKNSMKKXAKIKNVTPEPTRTPTPKVNLQPFNYEE IVSRGGNSHGGKKGNEEKMKEGLEDEKREEKALKNDXEERSLRGDVFFPKVNEAGEFGLILVQRKALTSKLEHKDLNISV DCSPNHGICDWKQDREDDFDWNPADRONAIGFYMAVPALAGHKKDIGRLKLLLPDLQPQSNFCLLFDYRLAGUKVGKLRV FVKNSNNALAWEKTTSEDEKWKTGKIQLYQGTDATKSIIFEAERGKGKTGEIAVDGVLLVSGLCPDSLLSVDD

(SEQ ID NO: 6)

EGFL6 (221-260 aa) 3D Model

EGF NMR Structure





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